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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/485,473

DATE: 09/10/2001  
TIME: 11:00:27

Input Set : A:\10496p61.app  
Output Set: R:\CRF3\09102001\I485473.raw

ENTERED

P.5

3 <110> APPLICANT: STOFFEL, WILHELM  
4 HOFMANN, KAY  
5 TOMIUK, STEPHAN  
7 <120> TITLE OF INVENTION: NEUTRAL SPHINGOMYELINASE  
9 <130> FILE REFERENCE: 10496/P61950US1  
11 <140> CURRENT APPLICATION NUMBER: 09/485,473  
12 <141> CURRENT FILING DATE: 2000-02-11  
14 <160> NUMBER OF SEQ ID NOS: 6  
16 <170> SOFTWARE: PatentIn Ver. 2.1  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 423  
20 <212> TYPE: PRT  
21 <213> ORGANISM: Homo sapiens  
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25 1 5 10 15  
27 Trp Gly Ile Pro Tyr Leu Ser Lys His Arg Ala Asp Arg Met Arg Arg  
28 20 25 30  
30 Leu Gly Asp Phe Leu Asn Gln Glu Ser Phe Asp Leu Ala Leu Leu Glu  
31 35 40 45  
33 Glu Val Trp Ser Glu Gln Asp Phe Gln Tyr Leu Arg Gln Lys Leu Ser  
34 50 55 60  
36 Pro Thr Tyr Pro Ala Ala His His Phe Arg Ser Gly Ile Ile Gly Ser  
37 65 70 75 80  
39 Gly Leu Cys Val Phe Ser Lys His Pro Ile Gln Glu Leu Thr Gln His  
40 85 90 95  
42 Ile Tyr Thr Leu Asn Gly Tyr Pro Tyr Met Ile His His Gly Asp Trp  
43 100 105 110  
45 Phe Ser Gly Lys Ala Val Gly Leu Leu Val Leu His Leu Ser Gly Met  
46 115 120 125  
48 Val Leu Asn Ala Tyr Val Thr His Leu His Ala Glu Tyr Asn Arg Gln  
49 130 135 140  
51 Lys Asp Ile Tyr Leu Ala His Arg Val Ala Gln Ala Trp Glu Leu Ala  
52 145 150 155 160  
54 Gln Phe Ile His His Thr Ser Lys Lys Ala Asp Val Val Leu Leu Cys  
55 165 170 175  
57 Gly Asp Leu Asn Met His Pro Glu Asp Leu Gly Cys Cys Leu Leu Lys  
58 180 185 190  
60 Glu Trp Thr Gly Leu His Asp Ala Tyr Leu Glu Thr Arg Asp Phe Lys  
61 195 200 205  
63 Gly Ser Glu Glu Gly Asn Thr Met Val Pro Lys Asn Cys Tyr Val Ser  
64 210 215 220  
66 Gln Gln Glu Leu Lys Pro Phe Pro Phe Gly Val Arg Ile Asp Tyr Val  
67 225 230 235 240  
69 Leu Tyr Lys Ala Val Ser Gly Phe Tyr Ile Ser Cys Lys Ser Phe Glu  
70 245 250 255  
72 Thr Thr Thr Gly Phe Asp Pro His Ser Gly Thr Pro Leu Ser Asp His

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Input Set : A:\0496p61.app  
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73          260          265          270
75 Glu Ala Leu Met Ala Thr Leu Phe Val Arg His Ser Pro Pro Gln Gln
76          275          280          285
78 Asn Pro Ser Ser Thr His Gly Pro Ala Glu Arg Ser Pro Leu Met Cys
79          290          295          300
81 Val Leu Lys Glu Ala Trp Thr Glu Leu Gly Leu Gly Met Ala Gln Ala
82 305          310          315          320
84 Arg Trp Trp Ala Thr Phe Ala Ser Tyr Val Ile Gly Leu Gly Leu Leu
85          325          330          335
87 Leu Leu Ala Leu Leu Cys Val Leu Ala Ala Gly Gly Gly Ala Gly Glu
88          340          345          350
90 Ala Ala Ile Leu Leu Trp Thr Pro Ser Val Gly Leu Val Leu Trp Ala
91          355          360          365
93 Gly Ala Phe Tyr Leu Phe His Val Gln Glu Val Asn Gly Leu Tyr Arg
94          370          375          380
96 Ala Gln Ala Glu Leu Gln His Val Leu Gly Arg Ala Arg Glu Ala Gln
97 385          390          395          400
99 Asp Leu Gly Pro Glu Pro Gln Pro Ala Leu Leu Leu Gly Gln Gln Glu
100          405          410          415
102 Gly Asp Arg Thr Lys Glu Gln
103          420
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 419
108 <212> TYPE: PRT
109 <213> ORGANISM: Murine sp.
111 <400> SEQUENCE: 2
112 Met Lys Leu Asn Phe Ser Leu Arg Leu Arg Val Phe Asn Leu Asn Cys
113 1          5          10          15
115 Trp Asp Ile Pro Tyr Leu Ser Lys His Arg Ala Asp Arg Met Lys Arg
116          20          25          30
118 Leu Gly Asp Phe Leu Asn Leu Glu Asn Phe Asp Leu Ala Leu Leu Glu
119          35          40          45
121 Glu Val Trp Ser Glu Gln Asp Phe Gln Tyr Leu Arg Gln Arg Leu Ser
122          50          55          60
124 Leu Thr Tyr Pro Asp Ala His Tyr Phe Arg Ser Gly Met Ile Gly Ser
125 65          70          75          80
127 Gly Leu Cys Val Phe Ser Lys His Pro Ile Gln Glu Ile Phe Gln His
128          85          90          95
130 Val Tyr Ser Leu Asn Gly Tyr Pro Tyr Met Phe His His Gly Asp Trp
131          100          105          110
133 Phe Cys Gly Lys Ser Val Gly Leu Leu Val Leu Arg Leu Ser Gly Leu
134          115          120          125
136 Val Leu Asn Ala Tyr Val Thr His Leu His Ala Glu Tyr Ser Arg Gln
137          130          135          140
139 Lys Asp Ile Tyr Phe Ala His Arg Val Ala Gln Ala Trp Glu Leu Ala
140 145          150          155          160
142 Gln Phe Ile His His Thr Ser Lys Asn Ala Asp Val Val Leu Leu Cys
143          165          170          175
145 Gly Asp Leu Asn Met His Pro Lys Asp Leu Gly Cys Cys Leu Leu Lys

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146          180          185          190
148 Glu Trp Thr Gly Leu His Asp Ala Phe Val Glu Thr Glu Asp Phe Lys
149          195          200          205
151 Gly Ser Asp Asp Gly Cys Thr Met Val Pro Lys Asn Cys Tyr Val Ser
152          210          215          220
154 Gln Gln Asp Leu Gly Pro Phe Pro Ser Gly Ile Arg Ile Asp Tyr Val
155 225          230          235          240
157 Leu Tyr Lys Ala Val Ser Glu Phe His Val Cys Cys Glu Thr Leu Lys
158          245          250          255
160 Thr Thr Thr Gly Cys Asp Pro His Ser Asp Lys Pro Phe Ser Asp His
161          260          265          270
163 Glu Ala Leu Met Ala Thr Leu Tyr Val Lys His Ser Pro Pro Gln Glu
164          275          280          285
166 Asp Pro Cys Thr Ala Cys Gly Pro Leu Glu Arg Ser Asp Leu Ile Ser
167          290          295          300
169 Val Leu Arg Glu Ala Arg Thr Glu Leu Gly Leu Gly Ile Ala Lys Ala
170 305          310          315          320
172 Arg Trp Trp Ala Ala Phe Ser Gly Tyr Val Ile Val Trp Gly Leu Ser
173          325          330          335
175 Leu Leu Val Leu Leu Cys Val Leu Ala Ala Gly Glu Glu Ala Arg Glu
176          340          345          350
178 Val Ala Ile Ile Leu Cys Ile Pro Ser Val Gly Leu Val Leu Val Ala
179          355          360          365
181 Gly Ala Val Tyr Leu Phe His Lys Gln Glu Ala Lys Gly Leu Cys Arg
182          370          375          380
184 Ala Gln Ala Glu Met Leu His Val Leu Thr Arg Glu Thr Glu Thr Gln
185 385          390          395          400
187 Asp Arg Gly Ser Glu Pro His Leu Ala Tyr Cys Leu Gln Gln Glu Gly
188          405          410          415
190 Asp Arg Ala
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 1662
195 <212> TYPE: DNA
196 <213> ORGANISM: Homo sapiens
198 <400> SEQUENCE: 3
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200 ggcgctctcc ggacccccag ggtcctagcg cgcggccctt accgagcctg ggcgcccgga 120
201 ttccggsagc ggatcgccctt tcggggttgg cgcccgccct gattgggaac agccggccgg 180
202 ttgccggggg aacgcgggag tcgggcccga cctgagccac cggggcttgg tgcccacctg 240
203 tgccgcgccg ctgcgaagaa ggaacgggtc agggagaagg cgccgcggcg ccccccgctg 300
204 cccacccggg ccgtcgctgg agagtctgag ccgcctagcg cccctggagc tcaccaacca 360
205 tgaagctcaa cttctccctg cgaactgcga tcttcaacct caactgctgg ggcattccgt 420
206 acttgagcaa gcaccgggcc gaccgcata ggcgcctggg agactttctg aaccaggaga 480
207 gcttcgacct ggccttgctg gaggaggtgt ggaagtgaaga ggaactccag tacctgagac 540
208 agaactgtgc acctacctac ccagctgcac accacttccg gagcggaatc attggcagtg 600
209 gcctctgtgt cttctccaaa catccaatcc aggaagctac ccagcacatc tacacttcca 660
210 atggtctacc ctacatgatc catcatggtg actggttcag tgggaaggct gtggggctcg 720
211 tgggtctcca ctaagtggc atggtgctca acgcctatgt gaccatctc catgcggaat 780
212 acaatcgaca gaaggacatc tacttagcac atcgtgtggc ccaagcttgg gaattggccc 840

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213 agttcatcca ccacacatcc aagaagcgag acgtggttct gttgtgtgga gacctcaaca 900
214 tgcaccocaga agacctgggc tgctgcctcg tgaaggagtg gacagggtct catgatgcct 960
215 atcttgaaac tcgggacttc aagggtctcg aggaaggcaa caaatgtgta cccaagaact 1020
216 gctacgtcag ccagcaggag ctgaagccat ttccctttgg tgctccgatt gactacgtgc 1080
217 tttaacaagg agtttctggg ttttacatct cctgtaagag ttttgaaacc actcaaggct 1140
218 ttgacctcca cagtggcacc cccctctctg atcatgaagc cctgatggct actctgtttg 1200
219 tgaggcacag cccccacag cagaacccca gctctaccca cggaccagca gagaggtcgc 1260
220 cgttgatgtg tgtgctaaag gaggcctgga cggagctggg tctgggcctg gctcaggctc 1320
221 gctgtggggc cacctctcgt agctatgtga ttggcctggg gctgctcttc ctggcactgc 1380
222 tgtgtgtcct ggcggctgga ggaggggccg gggaaagtgc catactgctc tggaccccca 1440
223 gtgtagggtc ggtgctgtgg gcaggtgcac tctacctctt ccacgtacag gaggtcaatt 1500
224 gcttatatag ggcccaggct gagctccagc atgtgctagg aaggggcaag gaggcccgag 1560
225 atctggggcc agagcctcag ccagccctac tctggggca gcaggagggg gacagaacta 1620
226 aagaacaata aagcttggcc ctttaaaaaa aaaaaaaaaa aa 1662
229 <210> SEQ ID NO: 4
230 <211> LENGTH: 1627
231 <212> TYPE: DNA
232 <213> ORGANISM: Murine sp.
234 <400> SEQUENCE: 4
235 gtgtgtgtgg aagccgagcc ggaacaaggg gaggaacctg taggcccggg tgcgagaacc 60
236 caccgaagagc ctaagaatct ggaacagtc acccgagatt ccttcaggga ctgccggcgg 120
237 ctccgcgacc agcccgggat ttgcagccga ccttctttcc ggggtgaaag acggcctttg 180
238 tcccagtaac gcaggagtgc cccccaccc ccaaccaagt cgcgttctgt ggtcggggca 240
239 gcgcaggaca gggcaataag cctgtgcgcy caatccgcct cgcgcgccct gctccgaagc 300
240 actccagcca tgaagctcaa cttttctcta cggctgagag ttttcaatct caactgctgt 360
241 gacatccctt acctgagcaa acataggggc gaccgcatga agcgccttgg agactttctg 420
242 aacttgaaaa actttgatct ggctctcctg gaggagggtg ggaagtgaac ggacttccag 480
243 tacttaagggc aaagcctatc gctcacctat ccagatgcac actacttcag aagcggtagt 540
244 ataggcagtg gcctctgtgt gttctccaaa caccataatc aggaatactt ccagcatgtc 600
245 tacagtctga atggttaccc ctacatgttc catcatggag actggttctg tgggaagtct 660
246 gtggggctgc tgggtctccg tctaagtgga ctggtgctca atgcctactg gactcatcta 720
247 catgctgagt caagcgacga gaaggacatc tactttgcac accgtgtggc ccaagcttgg 780
248 gaactggccc agttcatcca ccacacatcc aagaatgcag atgtggttct attgtgtgga 840
249 gacctcaata tgcaccccaa agacctgggc tgctgcctgc tgaaggagtg gacagggtct 900
250 catgatgctt tegttagaac tgaggacttt aagggtctgt atgatggctg taccatggtta 960
251 cccaagaact gctacgtcag ccagcaggac ctgggaccgt ttccgtctgg tatccggatt 1020
252 gttacgtgcg tttaacaaggc agtctctgag ttccacgtct gctgtgagac tctgaaacc 1080
253 actacaggct gtagacctca cagtgcacag ccttctctgt atcacagggc cctcatggct 1140
254 actttgtatg tgaagcacag ccccctcag gaagaccctt gtactgctg tggcccaact 1200
255 gaaaggctcc atttgatcag cgtgctaagg gaggccaagg cagagctggg gctagcgata 1260
256 gctaaagctc gctggtgggc tgcattctct ggcctatgtg tctgttgggg gctgtccctt 1320
257 tctggtgtgc gctgtgtcct ggctgcagga gaagaggcca gggaaagtgc catcatctc 1380
258 tgcattacca gtttgggtct ggtgctggtg gcaggtgac tctacctctt ccacaagcag 1440
259 gagcccaagg gcttatgtcg ggcccaggct gagatgctgc acgttctgac aagggaaacg 1500
260 gagccccagg accgaggctc agagcctcac ctgacctact gcttgacga ggagggggac 1560
261 agagcttaag agcttaacaa taaaacttgc ttgacacaca aaaaaaaaaa aaaaaaaaaa 1620
262 aaaaaaa
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 4464

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267 <212> TYPE: DNA  
268 <213> ORGANISM: Homo sapiens  
270 <220> FEATURE:  
271 <221> NAME/KEY: modified\_base  
272 <222> LOCATION: (2435)  
273 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
275 <220> FEATURE:  
276 <221> NAME/KEY: modified\_base  
277 <222> LOCATION: (2437)  
278 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
280 <220> FEATURE:  
281 <221> NAME/KEY: modified\_base  
282 <222> LOCATION: (2440)  
283 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
285 <220> FEATURE:  
286 <221> NAME/KEY: modified\_base  
287 <222> LOCATION: (3970)  
288 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
290 <220> FEATURE:  
291 <221> NAME/KEY: modified\_base  
292 <222> LOCATION: (4036)  
293 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
295 <220> FEATURE:  
296 <221> NAME/KEY: modified\_base  
297 <222> LOCATION: (4039)  
298 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
300 <220> FEATURE:  
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302 <222> LOCATION: (4045)  
303 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
305 <220> FEATURE:  
306 <221> NAME/KEY: modified\_base  
307 <222> LOCATION: (4076)  
308 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
310 <220> FEATURE:  
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312 <222> LOCATION: (4084)  
313 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
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316 <221> NAME/KEY: modified\_base  
317 <222> LOCATION: (4094)  
318 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
320 <220> FEATURE:  
321 <221> NAME/KEY: modified\_base  
322 <222> LOCATION: (4102)  
323 <223> OTHER INFORMATION: a, t, c, g, other or unknown  
325 <220> FEATURE:  
326 <221> NAME/KEY: modified\_base  
327 <222> LOCATION: (4103)

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\10496p61.app

Output Set: N:\CRF3\09102001\I485473.raw

L:546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:579 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6